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SEQUENCE LISTING

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<120> MOLECULES INHIBITING HEPATITIS C VIRUS PROTEIN SYNTHESIS AND
METHOD FOR SCREENING SAME

<130> 1759.200

<150> PCT/FR03/03675

<151> 2003-12-11

<150> FR0215718

<151> 2002-12-12

<160> 16

<170> PatentIn version 3.1

<210> 1

<211> 326

<212> DNA

<213> Artificial Sequence

<220><221> HCV

<222> 40..372

<223> corresponds to IRES sequence of HCV

<400> 1

ctccccctgtg aagaactact gtcttcacgc agaaagcgct tagccatggc gtttagtatga 60

gtgtcgtgca gcctccagga ccccccctcc cgggagagcc atagtggtct gcggAACCGG 120

ttagtacacc ggaattgcca ggatgaccgg gtcctttctt ggtcaaccc gctcaatgcc 180

tggagatttg ggcgtcccc cgcgagactg ctagccgagt agtgttgggt cgcgaaaggc 240

cttgtggtagc tgcctgatag ggtgcttgcg agtgccccgg gaggtctcgt agaccgtgca 300

tcatgagcac aaatcctaaa gaaaaaa 326

<210> 2

<211> 80

<212> DNA

<213> Artificial Sequence

<220><221> HCV

<222> 40..119

<223> corresponds to a portion (region II) of HCV IRES sequence

<400> 2
 ctccccctgtg aggaactact gtcttcacgc agaaagcgta tagccatggc gtttagtatga 60
 gtgttgtgca gcctccagga 80

<210> 3
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220><221> HCV
 <222> 56..92
 <223> corresponds to a portion (consensus sequence) of HCV IRES sequence

<400> 3
 tactgtcttc acgcagaaaag cgtcttagcca tggcggt 37

<210> 4
 <211> 814
 <212> PRT
 <213> Artificial Sequence

<220><221> p116
 <222> 1..814
 <223> corresponds to p116 subunit of eIF3

<400> 4
 Met Gln Asp Ala Glu Asn Val Ala Val Pro Glu Ala Ala Glu Glu Arg
 1 5 10 15

Ala Glu Pro Gly Gln Gln Gln Pro Ala Ala Glu Pro Pro Pro Ala Glu
 20 25 30

Gly Leu Leu Arg Pro Ala Gly Pro Gly Ala Pro Glu Ala Ala Gly Thr
 35 40 45

Glu Ala Ser Ser Glu Glu Val Gly Ile Ala Glu Ala Gly Pro Glu Pro
 50 55 60

Glu Val Arg Thr Glu Pro Ala Ala Glu Ala Ala Ser Gly Pro
 65 70 75 80

Ser Glu Ser Pro Ser Pro Pro Ala Ala Glu Glu Leu Pro Gly Ser His
85 90 95

Ala Glu Pro Pro Val Pro Ala Gln Gly Glu Ala Pro Gly Glu Gln Ala
100 105 110

Arg Asp Glu Arg Ser Asp Ser Arg Ala Gln Ala Val Ser Glu Asp Ala
115 120 125

Gly Gly Asn Glu Gly Arg Ala Ala Glu Ala Glu Pro Arg Ala Leu Glu
130 135 140

Asn Gly Asp Ala Asp Glu Pro Ser Phe Ser Asp Pro Glu Asp Phe Val
145 150 155 160

Asp Asp Val Ser Glu Glu Leu Leu Gly Asp Val Leu Lys Asp Arg
165 170 175

Pro Gln Glu Ala Asp Gly Ile Asp Ser Val Ile Val Val Asp Asn Val
180 185 190

Pro Gln Val Gly Pro Asp Arg Leu Glu Lys Leu Lys Asn Val Ile His
195 200 205

Lys Ile Phe Ser Lys Phe Gly Lys Ile Thr Asn Asp Phe Tyr Pro Glu
210 215 220

Glu Asp Gly Lys Thr Lys Gly Tyr Ile Phe Leu Glu Tyr Ala Ser Pro
225 230 235 240

Ala His Ala Val Asp Ala Val Lys Asn Ala Asp Gly Tyr Lys Leu Asp
245 250 255

Lys Gln His Thr Phe Arg Val Asn Leu Phe Thr Asp Phe Asp Lys Tyr
260 265 270

Met Thr Ile Ser Asp Glu Trp Asp Ile Pro Glu Lys Gln Pro Phe Lys
275 280 285

Asp Leu Gly Asn Leu Arg Tyr Trp Leu Glu Glu Ala Glu Cys Arg Asp
290 295 300

Gln Tyr Ser Val Ile Phe Glu Ser Gly Asp Arg Thr Ser Ile Phe Trp
305 310 315 320

Asn Asp Val Lys Asp Pro Val Ser Ile Glu Glu Arg Ala Arg Trp Thr
325 330 335

Glu Thr Tyr Val Arg Trp Ser Pro Lys Gly Thr Tyr Leu Ala Thr Phe
340 345 350

His Gln Arg Gly Ile Ala Leu Trp Gly Gly Glu Lys Phe Lys Gln Ile
355 360 365

Gln Arg Phe Ser His Gln Gly Val Gln Leu Ile Asp Phe Ser Pro Cys
370 375 380

Glu Arg Tyr Leu Val Thr Phe Ser Pro Leu Met Asp Thr Gln Asp Asp
385 390 395 400

Pro Gln Ala Ile Ile Ile Trp Asp Ile Leu Thr Gly His Lys Lys Arg
405 410 415

Gly Phe His Cys Glu Ser Ser Ala His Trp Pro Ile Phe Lys Trp Ser
420 425 430

His Asp Gly Lys Phe Phe Ala Arg Met Thr Leu Asp Thr Leu Ser Ile
435 440 445

Tyr Glu Thr Pro Ser Met Gly Leu Leu Asp Lys Lys Ser Leu Lys Ile
450 455 460

Ser Gly Ile Lys Asp Phe Ser Trp Ser Pro Gly Gly Asn Ile Ile Ala
465 470 475 480

Phe Trp Val Pro Glu Asp Lys Asp Ile Pro Ala Arg Val Thr Leu Met
485 490 495

Gln Leu Pro Thr Arg Gln Glu Ile Arg Val Arg Asn Leu Phe Asn Val
500 505 510

Val Asp Cys Lys Leu His Trp Gln Lys Asn Gly Asp Tyr Leu Cys Val
515 520 525

Lys Val Asp Arg Thr Pro Lys Gly Thr Gln Gly Val Val Thr Asn Phe
530 535 540

Glu Ile Phe Arg Met Arg Glu Lys Gln Val Pro Val Asp Val Val Glu
545 550 555 560

Met Lys Glu Thr Ile Ile Ala Phe Ala Trp Glu Pro Asn Gly Ser Lys
565 570 575

Phe Ala Val Leu His Gly Glu Ala Pro Arg Ile Ser Val Ser Phe Tyr
580 585 590

His Val Lys Asn Asn Gly Lys Ile Glu Leu Ile Lys Met Phe Asp Lys
595 600 605

Gln Gln Ala Asn Thr Ile Phe Trp Ser Pro Gln Gly Gln Phe Val Val
610 615 620

Leu Ala Gly Leu Arg Ser Met Asn Gly Ala Leu Ala Phe Val Asp Thr
625 630 635 640

Ser Asp Cys Thr Val Met Asn Ile Ala Glu His Tyr Met Ala Ser Asp
645 650 655

Val Glu Trp Asp Pro Thr Gly Arg Tyr Val Val Thr Ser Val Ser Trp
660 665 670

Trp Ser His Lys Val Asp Asn Ala Tyr Trp Leu Trp Thr Phe Gln Gly
675 680 685

Arg Leu Leu Gln Lys Asn Asn Lys Asp Arg Phe Cys Gln Leu Leu Trp
690 695 700

Arg Pro Arg Pro Pro Thr Leu Leu Ser Gln Glu Gln Ile Lys Gln Ile
705 710 715 720

Lys Lys Asp Leu Lys Lys Tyr Ser Lys Ile Phe Glu Gln Lys Asp Arg
725 730 735

Leu Ser Gln Ser Lys Ala Ser Lys Glu Leu Val Glu Arg Arg Arg Thr
740 745 750

Met Met Glu Asp Phe Arg Lys Tyr Arg Lys Met Ala Gln Glu Leu Tyr
755 760 765

Met Glu Gln Lys Asn Glu Arg Leu Glu Leu Arg Gly Gly Val Asp Thr
770 775 780

Asp Glu Leu Asp Ser Asn Val Asp Asp Trp Glu Glu Glu Thr Ile Glu
785 790 795 800

Phe Phe Val Thr Glu Glu Ile Ile Pro Leu Gly Asn Gln Glu
805 810

<210> 5
<211> 106
<212> PRT
<213> Artificial Sequence

<220><221> p116
<222> 175..279
<223> corresponds to a portion (RRM) of eIF3 p116 subunit

<400> 5

Met Asp Arg Pro Gln Glu Ala Asp Gly Ile Asp Ser Val Ile Val Val
1 5 10 15

Asp Asn Val Pro Gln Val Gly Pro Asp Arg Leu Glu Lys Leu Lys Asn
20 25 30

Val Ile His Lys Ile Phe Ser Lys Phe Gly Lys Ile Thr Asn Asp Phe
35 40 45

Tyr Pro Glu Glu Asp Gly Lys Thr Lys Gly Tyr Ile Phe Leu Glu Tyr
50 55 60

Ala Ser Pro Ala His Ala Val Asp Ala Val Lys Asn Ala Asp Gly Tyr
65 70 75 80

Lys Leu Asp Lys Gln His Thr Phe Arg Val Asn Leu Phe Thr Asp Phe
85 90 95

Asp Lys Tyr Met Thr Ile Ser Asp Glu Trp
100 105

<210> 6
<211> 33
<212> DNA
<213> Artificial Sequence

<220><221> primer_bind
<222> 1..33
<223> HCV RRM 5' primer (RRMfwd)

<400> 6

catatggatc ggccccagga agcagatgga atc 33

<210> 7
<211> 33
<212> DNA
<213> Artificial Sequence

<220><221> primer_bind
<222> 1..33
<223> HCV RRM 3' primer (RRMrev)

<400> 7

gtgctcgagc cactcgtcac tgatcgatata 33

<210> 8
<211> 29
<212> DNA
<213> Artificial Sequence

<220><221> primer_bind
<222> 1..29

<223> HCV IRES 5' primer (IRESfwd)

<400> 8

accgctagcc tccccctgtga ggaactact

29

<210> 9

<211> 46

<212> DNA

<213> Artificial Sequence

<220><221> primer_bind

<222> 1..46

<223> HCV IRES 3' primer (IRESrev)

<400> 9

gaaagctttt ttctttgagg ttttaggattt gtgctcatga tgcacg

46

<210> 10

<211> 95

<212> DNA

<213> Artificial Sequence

<220><221> primer_bind

<222> 1..95

<223> primer IIIabcfwd which corresponds to T7 polymerase promoter + 139-215 of HCV (regions IIIa-IIIb)

<400> 10

taatacgact cactataggg tagtggtctg cggaaccgggt gagtacaccg gaattgccag 60

gacgaccgggg tcctttcttg gataaaacccg ctcaa 95

<210> 11

<211> 60

<212> DNA

<213> Artificial Sequence

<220><221> primer_bind

<222> 1..60

<223> primer IIIabcrev which corresponds to 193-252 of HCV (regions IIIb-IIIc)

<400> 11

tagcagtctc gcgggggcac gcccaaatct ccaggcattg agcgggttga tccaagaaag 60

<210> 12
<211> 20
<212> DNA
<213> Artificial Sequence

<220><221> primer_bind
<222> 1..20
<223> primer T7 which corresponds to a portion of primer IIIabcfwd

<400> 12

taatacgact cactataggg 20

<210> 13
<211> 21
<212> DNA
<213> Artificial Sequence

<220><221> primer_bind
<222> 1..21
<223> primer which corresponds to a portion of primer IIIabcrev

<400> 13

tagcagtctc gcgggggcac g 21

<210> 14
<211> 22
<212> DNA
<213> Artificial Sequence

<220><221> primer_bind
<222> 1..22
<223> primer SP6

<400> 14

tatttaggtg acactataga at 22

<210> 15
<211> 27
<212> DNA
<213> Artificial Sequence

<220><221> primer_bind
<222> 1..27
<223> primer Linkerrev

<400> 15

gtcctggtgg ctgcaggaca ctcatac

27

<210> 16
<211> 48
<212> DNA
<213> Artificial Sequence

<220><221> primer_bind
<222> 1..48
<223> primer LinkerSP6

<400> 16

tatttagtg acactataga atactcaagc tatgcattca acgcgttg

48